

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: SmithKline Beecham, Corporation
- (ii) TITLE OF INVENTION: Recombinant Feline Coronavirus S Proteins
- (iii) NUMBER OF SEQUENCES: 54
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: SmithKline Beecham Corporation
  - (B) STREET: 709 Swedeland Road
  - (C) CITY: King of Prussia
  - (D) STATE: PA
  - (E) COUNTRY: USA
  - (F) ZIP: 19406-2799
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE:
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/698,927
  - (B) FILING DATE: 13-MAY-1991
- (viii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 07/613,066
  - (B) FILING DATE: 14-NOV-1990
- (ix) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: King, William T.
  - (B) REGISTRATION NUMBER: 30,954
  - (C) REFERENCE/DOCKET NUMBER: SBC 14532B
- (x) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (215) 270-5015
  - (B) TELEFAX: (215) 270-5090

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

G TGCCCCCGG GTATGATTGT GCTCGTACT TGCCTCTTG

## (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AAATACCCGG GCACTGGTAA TGCACGTGGT AAACC

35

## (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 35 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTATTCCCGG GCACGCTCAA GCACTGCTAC CTGGG

35

## (2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 36 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGATCCCGG GGTACAATCT GGTATGGGTG CTACAG

36

## (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCTTACCCGG GGTGGTTATG GTCAACCCAT AGCCTCGAC

39

## (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 39 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGTGACCCGG GCGCCATGTG ATGTAAGCGC ACAAGCGGC

39

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCAATCCCGG GGGGTGCCAG ACTTGAAAAC ATGGAGG

37

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTACCCGG GGGTGCACTT GGTGGTGGCG CCGTGGC

37

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TAGGTCCCGG GCTCAGTCTC AGAGATTGG ATTCTGTGG

39

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATAATAGGCC TGGTTTACCA CGTGCATTAC CAGTGC

36

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 35 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTATTAGGCC TCCCAGGTAG CAGTGCTTGA GCGTG

35

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 36 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AAATAAGGCC TCTGTAGCAC CCATACCAGA TTGTAC

36

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA (genomic)
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTAGTAGGCC TGTGAGGGCT ATGGGTTGAC CATAACCAC

39

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 39 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAACAAGGCC TGCCGCTTGT GCGCTTACAT CACATGGCG

39

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATCAAAGGCC TCCTCCATGT TTTCAAGTCT GGCAACC

37

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTATAAGGCC TGCCACGGCG CCACCAACAA GTGCACC

37

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CATTAAGGCC TCCACAGAAC CGGAATCTCT GAGACTGAG

39

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

TAAATAGGCC TTTAGTGGAC ATGCACCTTT TCAATTGG

38

## (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 573 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

ATG GAT CCC GAA TTC CAA GAA AAA ACA CAA TCT CTG TTT GCC AAC GCA	48
Met Asp Pro Glu Phe Gln Glu Lys Thr Gln Ser Leu Phe Ala Asn Ala	
1                   5                   10                   15	
TTT GGC TAC CCT GCC ACT CAC ACC ATT CAG GGC CCT GGC CGC GTG AAT	96
Phe Gly Tyr Pro Ala Thr His Thr Ile Gln Gly Pro Gly Arg Val Asn	
20                   25                   30	
TTG ATT GGT GAA CAC ACC GAC TAC AAC GAC GGT TTC GTT CTG CCC TGC	144
Leu Ile Gly Glu His Thr Asp Tyr Asn Asp Gly Phe Val Leu Pro Cys	
35                   40                   45	
GCG ATT GAT TAT CAA ACC GTG ATC CCT AAT ACC CGG GGC ACT GGT AAT	192
Ala Ile Asp Tyr Gln Thr Val Ile Pro Asn Thr Arg Gly Thr Gly Asn	
50                   55                   60	
GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG CCT GTT AGT	240
Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val Ser	
65                   70                   75                   80	
GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA CAA AGG CCC	288
Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg Pro	
85                   90                   95	
CTT TTA AAA CAT GGG TTA GTG TGT ATA ACT AAA AAT CGC CAT ATT AAC	336
Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile Asn	
100                   105                   110	
TAT GAA CAA TTC GCC TCC AAC CAG TGG AAT TCC ACA TGT ACG GGT GCT	384
Tyr Glu Gln Phe Ala Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly Ala	
115                   120                   125	
GAC AGA AAA ATT CCC TTC TCT GTC ATA CCC ACG GAC AAT GGA ACA AAA	432
Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr Lys	
130                   135                   140	
ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT TAT ATT AGT	480
Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile Ser	
145                   150                   155                   160	
GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT AAC AAT GTC	528
Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn Val	
165                   170                   175	
ACA CTT TTG TAT TCA CGC AGC AGC ACT GCT ACC TGG GAG GCC	570
Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu Ala	
180                   185                   190	
TAG	573

## (2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Met	Asp	Pro	Glu	Phe	Gln	Glu	Lys	Thr	Gln	Ser	Leu	Phe	Ala	Asn	Ala
1				5				10						15	
Phe	Gly	Tyr	Pro	Ala	Thr	His	Thr	Ile	Gln	Gly	Pro	Gly	Arg	Val	Asn
	20					25							30		
Leu	Ile	Gly	Glu	His	Thr	Asp	Tyr	Asn	Asp	Gly	Phe	Val	Leu	Pro	Cys
		35				40							45		
Ala	Ile	Asp	Tyr	Gln	Thr	Val	Ile	Pro	Asn	Thr	Arg	Gly	Thr	Gly	Asn
	50				55					60					
Ala	Arg	Gly	Lys	Pro	Leu	Leu	Phe	His	Val	Gly	Glu	Pro	Val	Ser	
	65				70				75			80			
Val	Ile	Ile	Tyr	Ile	Ser	Ala	Tyr	Arg	Asp	Asp	Val	Gln	Gln	Arg	Pro
		85					90						95		
Leu	Leu	Lys	His	Gly	Leu	Val	Cys	Ile	Thr	Lys	Asn	Arg	His	Ile	Asn
		100				105						110			
Tyr	Glu	Gln	Phe	Ala	Ser	Asn	Gln	Trp	Asn	Ser	Thr	Cys	Thr	Gly	Ala
	115					120					125				
Asp	Arg	Lys	Ile	Pro	Phe	Ser	Val	Ile	Pro	Thr	Asp	Asn	Gly	Thr	Lys
	130				135						140				
Ile	Tyr	Gly	Leu	Glu	Trp	Asn	Asp	Asp	Phe	Val	Thr	Ala	Tyr	Ile	Ser
	145			150				155					160		
Gly	Arg	Ser	Tyr	His	Leu	Asn	Ile	Asn	Thr	Asn	Trp	Phe	Asn	Asn	Val
	165					170							175		
Thr	Leu	Leu	Tyr	Ser	Arg	Ser	Ser	Thr	Ala	Thr	Trp	Glu	Ala		
	180					185						190			

## (2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4365 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..4362

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATG ATT GTG CTC GTA ACT TGC CTC TTG TTG TTA TGT TCA TAC CAC ACA Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr 1 5 10 15	48
GTT TTG AGT ACA ACA AAT AAT GAA TGC ATA CAA GTT AAC GTA ACA CAA Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln 20 25 30	96
TTG GCT GGC AAT GAA AAC CTT ATC AGA GAT TTT CTG TTT AGT AAC TTT Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe 35 40 45	144
AAA GAA GAA GGA AGT GTA GTT GGT GGT TAT TAC CCT ACA CAG GTG Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val 50 55 60	192
TGG TAC AAC TGC TCT AGA ACA GCA CAA ACT ACT GCC TTT CAG TAT TTT Trp Tyr Asn Cys Ser Arg Thr Ala Gln Thr Thr Ala Phe Gln Tyr Phe 65 70 75 80	240
AAT AAT ATA CAT GCC TTT TAT TTT GTT ATG GAA GCC ATG GAA AAT AGC Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser 85 90 95	288
ACT GGT AAT GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu 100 105 110	336
CCT GTT AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln 115 120 125	384
CAA AGG CCC CTT TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg 130 135 140	432
CAT ATT AAC TAT GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys 145 150 155 160	480
ACG GGT GCT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn 165 170 175	528
GGA ACA AAA ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala 180 185 190	576
TAT ATT AGT GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe 195 200 205	624
AAC AAT GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GAA Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu 210 215 220	672
TAC AGT GCT GCA TAT GCT TAC CAA GGT GTT TCT AAC TTC ACT TAT TAC Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr 225 230 235 240	720
AAG TTA AAT AAC ACC AAT GGT CTA AAA ACC TAT GAA TTA TGT GAA GAT Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp 245 250 255	768

TAT GAA CAT TGC ACT GGC TAT GCT ACC AAT GTA TTT GCT CCG ACA TCA Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser 260 265 270	816
GGT GGT TAC ATA CCT GAT GGA TTT AGT TTT AAC AAT TGG TTC TTG CTT Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu 275 280 285	864
ACA AAT AGT TCC ACT TTT GTT AGT GGC AGG TTT GTA ACA AAT CAA CCA Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro 290 295 300	912
TTA TTG ATT AAT TGC TTG TGG CCA GTG CCC AGT TTT GGT GTA GCA GCA Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala 305 310 315 320	960
CAA GAA TTT TGT TTT GAA GGT GCA CAG TTT AGC CAA TGT AAT GGT GTG Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val 325 330 335	1008
TCT TTA AAT AAC ACA GTG GAT GTT ATT AGA TTC AAC CTT AAT TTC ACT Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr 340 345 350	1056
GCA GAT GTA CAA TCT GGT ATG GGT GCT ACA GTA TTT TCA CTG AAT ACA Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr 355 360 365	1104
ACA GGT GGT GTC ATT CTT GAA ATT TCA TGT TAT AGT GAC ACA GTG AGT Thr Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser 370 375 380	1152
GAG TCT AGT TCT TAC AGT TAT GGT GAA ATC CCG TTC GGC ATA ACT GAC Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp 385 390 395 400	1200
GGA CCA CGA TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAA TAT Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr 405 410 415	1248
TTA GGA ACA TTA CCA CCC AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp 420 425 430	1296
GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445	1344
GGT TGT ATA TCT TTT AAT TTA ACC ACT GGT GCT AGT GGA GCT TTT TGG Gly Cys Ile Ser Phe Asn Leu Thr Thr Gly Ala Ser Gly Ala Phe Trp 450 455 460	1392
ACA ATT GCT TAC ACA TCG TAT ACT GAA GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480	1440
ACA GCT ATT AAA AAT GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495	1488
AAA TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510	1536
GCT TCA AGT GAA GTA GGT TTC GTT AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525	1584

AGC TTT TTC ACA CAC ACC GCT GTC AAT ATA ACC ATT GAT CTT GGT ATG Ser Phe Phe Thr His Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met 530 535 540	1632
AAG CTT AGT GGT TAT GGT CAA CCC ATA GCC TCG ACA CTA AGT AAC ATC Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560	1680
ACA CTA CCA ATG CAG GAT AAC AAT ACT GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575	1728
AAC CAA TTC TCA GTT TAT GTT CCT TCC ACT TGC AAA AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val Pro Ser Thr Cys Lys Ser Ser Leu Trp 580 585 590	1776
GAC AAT ATT TTT AAT CAA GAC TGC ACG GAT GTT TTA GAG GCT ACA GCT Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala 595 600 605	1824
GTT ATA AAA ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn 610 615 620	1872
TAC TTG ACT TTT AAC AAG TTC TGT TTG TCG TTG AGT CCT GTT GGT GCT Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640	1920
AAT TGC AAG TTT GAT GTT GCT GCA CGT ACA AGA ACC AAT GAG CAG GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655	1968
GTT AGA AGT CTA TAT GTA ATA TAT GAA GAA GGA GAC AAC ATA GTG GGT Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670	2016
GTA CCG TCT GAT AAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asn Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685	2064
GAC TCC TGT ACA GAT TAC AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700	2112
ATT AGA CGA ACT AAC AGT ACC CTA CTT AGT GGC TTA TAT TAC ACA TCA Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser 705 710 715 720	2160
CTA TCA GGT GAT TTG TTA GGC TTT AAA AAT GTT AGT GAT GGT GTC ATT Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile 725 730 735	2208
TAT TCT GTG ACG CCA TGT GAT GTA AGC GCA CAA GCG GCT GTT ATT GAT Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp 740 745 750	2256
GGT GCC ATA GTT GGA GCT ATG ACT TCC ATT AAC AGT GAA CTG TTA GGT Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly 755 760 765	2304
CTA ACA CAT TGG ACA ACG ACA CCT AAT TTT TAT TAC TAC TCT ATA TAT Leu Thr His Trp Thr Thr Pro Asn Phe Tyr Tyr Ser Ile Tyr 770 775 780	2352
AAT TAC ACA AGT GAG AGG ACT CGT GGC ACT GCA ATT GAC AGT AAC GAT Asn Tyr Thr Ser Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp 785 790 795 800	2400

GTT GAT TGT GAA CCT GTC ATA ACC TAT TCT AAT ATA GGT GTT TGT AAA Val Asp Cys Glu Pro Val Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys 805	810	815	2448
AAT GGT GCT TTG TTT ATT AAC GTC ACA CAT TCT GAC GGA GAC GTG Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val 820	825	830	2496
CAA CCA ATT AGC ACT GGT AAT GTC ACG ATA CCT ACA AAT TTT ACC ATA Gln Pro Ile Ser Thr Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile 835	840	845	2544
TCT GTG CAA GTT GAA TAC ATG CAG GTT TAC ACT ACA CCA GTA TCA ATA Ser Val Gln Val Glu Tyr Met Gln Val Tyr Thr Pro Val Ser Ile 850	855	860	2592
GAT TGT GCA AGA TAC GTT TGT AAT GGT AAC CCT AGA TGT AAC AAA TTG Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu 865	870	875	2640
TTA ACA CAA TAT GTG TCT GCA TGT CAA ACT ATT GAA CAA GCA CTT GCA Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala 885	890	895	2688
ATG GGT GCC AGA CTT GAA AAC ATG GAG GTT GAT TCC ATG TTG TTT GTC Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val 900	905	910	2736
TCG GAA AAT GCC CTT AAA TTG GCA TCT GTT GAG GCG TTC AAT AGT ACA Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr 915	920	925	2784
GAA AAT TTA GAT CCT ATT TAC AAA GAA TGG CCT AGC ATA GGT GGT TCT Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Ser Ile Gly Gly Ser 930	935	940	2832
TGG CTA GGA GGT CTA AAA GAT ATA CTA CCG TCC CAT AAT AGC AAA CGT Trp Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg 945	950	955	2880
AAG TAT GGT TCT GCT ATA GAA GAT TTG CTT TTT GAT AAA GTT GTA ACA Lys Tyr Gly Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr 965	970	975	2928
TCT GGT TTA GGT ACA GTT GAT GAA GAT TAT AAA CGT TGT ACT GGT GGT Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly 980	985	990	2976
TAC GAC ATA GCA GAC TTG GTG TGT GCT CAA TAT TAC AAT GGC ATC ATG Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Asn Gly Ile Met 995	1000	1005	3024
GTT CTA CCA GGT GTA GCT AAT GCT GAC AAG ATG ACT ATG TAC ACA GCA Val Leu Pro Gly Val Ala Asn Ala Asp Lys Met Thr Met Tyr Thr Ala 1010	1015	1020	3072
TCA CTT GCA GGT GGT ATA ACA TTA GGT GCA CTT GGT GGT GGC GCC GTG Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Ala Val 1025	1030	1035	3120
GCT ATA CCT TTT GCA GTA GCA GTC CAG GCT AGA CTT AAT TAT GTT GCT Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala 1045	1050	1055	3168
CTA CAA ACT GAT GTA TTG AAT AAA AAC CAA CAG ATC CTG GCT AAT GCT Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala 1060	1065	1070	3216

TTC AAT CAA GCT ATT GGT AAC ATT ACA CAG GCT TTT GGT AAG GTT AAT Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn 1075 1080 1085	3264
GAT GCT ATA CAT CAA ACA TCA CAA GGT CTT GCC ACT GTT GCT AAA GCG Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala Thr Val Ala Lys Ala 1090 1095 1100	3312
TTG GCA AAA GTG CAA GAT GTT GTC AAC ACA CAA GGG CAA GCT TTA AGT Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser 1105 1110 1115 1120	3360
CAC CTT ACA GTA CAA TTG CAA AAT AAT TTT CAA GCC ATT AGT AGT TCT His Leu Thr Val Gln Leu Asn Asn Phe Gln Ala Ile Ser Ser Ser 1125 1130 1135	3408
ATT AGT GAT ATT TAT AAC AGG CTT GAC GAA CTG AGT GCT GAT GCA CAA Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln 1140 1145 1150	3456
GTT GAT AGG CTG ATT ACA GGT AGA CTT ACA GCA CTT AAT GCA TTT GTG Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val 1155 1160 1165	3504
TCT CAG ACT CTA ACC AGA CAA GCA GAG GTT AGG GCT AGT AGA CAA CTT Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu 1170 1175 1180	3552
GCC AAA GAC AAG GTT AAT GAA TGT GTT AGG TCT CAG TCT CAG AGA TTC Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe 1185 1190 1195 1200	3600
GGA TTC TGT GGT AAT GGT ACA CAT TTG TTT TCA CTA GCA AAT GCA GCA Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala 1205 1210 1215	3648
CCA AAT GGC ATG ATT TTC TTT CAT ACA GTA CTA TTA CCA ACA GCT TAT Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr 1220 1225 1230	3696
GAA ACT GTA ACA GCT TGG TCA GGT ATT TGT GCT TCA GAT GGC GAT CGC Glu Thr Val Thr Ala Trp Ser Gly Ile Cys Ala Ser Asp Gly Asp Arg 1235 1240 1245	3744
ACT TTC GGA CTT GTC GTT AAA GAT GTG CAG TTG ACG TTG TTT CGT AAT Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn 1250 1255 1260	3792
CTA GAT GAC AAG TTC TAT TTG ACC CCC AGA ACT ATG TAT CAG CCT AGA Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg 1265 1270 1275 1280	3840
GTT GCA ACT AGT TCT GAT TTT GTT CAA ATT GAA GGG TGT GAT GTG TTG Val Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu 1285 1290 1295	3888
TTT GTC AAC GCG ACT GTA ATT GAT TTG CCT AGT ATT ATA CCT GAC TAT Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr 1300 1305 1310	3936
ATT GAC ATT AAT CAA ACT GTT CAA GAC ATA TTA GAA AAT TAC AGA CCA Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro 1315 1320 1325	3984
AAC TGG ACT GTA CCT GAA TTT ACA CTT GAT ATT TTC AAC GCA ACC TAT Asn Trp Thr Val Pro Glu Phe Thr Leu Asp Ile Phe Asn Ala Thr Tyr 1330 1335 1340	4032

TTA AAT CTG ACT GGT GAA ATT GAT GAC TTA GAG TTT AGG TCA GAA AAG Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys 1345 1350 1355 1360	4080
CTA CAT AAC ACT ACA GTA GAA CTT GCC ATT CTC ATT GAT ACC ATT AAT Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Thr Ile Asn 1365 1370 1375	4128
AAT ACA TTA GTC AAT CTT GAA TGG CTC AAT AGA ATT GAA ACT TAT GTA Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val 1380 1385 1390	4176
AAA TGG CCT TGG TAT GTG TGG CTA CTG ATA GGT CTA GTA GTA GTA TTT Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Val Phe 1395 1400 1405	4224
TGC ATA CCA TTA CTG CTA TTT TGC TGT TTT AGC ACA GGT TGT TGT GGA Cys Ile Pro Leu Leu Phe Cys Cys Phe Ser Thr Gly Cys Cys Gly 1410 1415 1420	4272
TGC ATA GGT TGT TTA GGA AGT TGT TGT CAC TCT ATA TGT AGT AGA AGA Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg 1425 1430 1435 1440	4320
CAA TTT GAA TAT TAT GAA CCA ATT GAA AAA GTG CAT GTC CAC Gln Phe Glu Tyr Tyr Glu Pro Ile Glu Lys Val His Val His 1445 1450	4362
<b>TAA</b>	<b>4365</b>

## (2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1454 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr 1 5 10 15
Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln 20 25 30
Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe 35 40 45
Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val 50 55 60
Trp Tyr Asn Cys Ser Arg Thr Ala Gln Thr Thr Ala Phe Gln Tyr Phe 65 70 75 80
Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser 85 90 95
Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu 100 105 110
Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln 115 120 125

Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg  
 130 135 140  
 His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys  
 145 150 155 160  
 Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn  
 165 170 175  
 Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala  
 180 185 190  
 Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe  
 195 200 205  
 Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu  
 210 215 220  
 Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr  
 225 230 235 240  
 Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp  
 245 250 255  
 Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser  
 260 265 270  
 Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu  
 275 280 285  
 Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro  
 290 295 300  
 Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala  
 305 310 315 320  
 Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val  
 325 330 335  
 Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr  
 340 345 350  
 Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr  
 355 360 365  
 Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser  
 370 375 380  
 Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp  
 385 390 395 400  
 Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr  
 405 410 415  
 Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp  
 420 425 430  
 Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile  
 435 440 445  
 Gly Cys Ile Ser Phe Asn Leu Thr Thr Gly Ala Ser Gly Ala Phe Trp  
 450 455 460  
 Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn  
 465 470 475 480

Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile  
485 490 495

Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val  
500 505 510

Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro  
515 520 525

Ser Phe Phe Thr His Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met  
530 535 540

Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile  
545 550 555 560

Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser  
565 570 575

Asn Gln Phe Ser Val Tyr Val Pro Ser Thr Cys Lys Ser Ser Leu Trp  
580 585 590

Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala  
595 600 605

Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn  
610 615 620

Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala  
625 630 635 640

Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val  
645 650 655

Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly  
660 665 670

Val Pro Ser Asp Asn Ser Gly Leu His Asp Leu Ser Val Leu His Leu  
675 680 685

Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile  
690 695 700

Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser  
705 710 715 720

Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile  
725 730 735

Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp  
740 745 750

Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly  
755 760 765

Leu Thr His Trp Thr Thr Pro Asn Phe Tyr Tyr Ser Ile Tyr  
770 775 780

Asn Tyr Thr Ser Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp  
785 790 795 800

Val Asp Cys Glu Pro Val Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys  
805 810 815

Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val  
820 825 830

Gln Pro Ile Ser Thr Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile  
 835 840 845  
 Ser Val Gln Val Glu Tyr Met Gln Val Tyr Thr Pro Val Ser Ile  
 850 855 860  
 Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu  
 865 870 875 880  
 Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala  
 885 890 895  
 Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val  
 900 905 910  
 Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr  
 915 920 925  
 Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Ser Ile Gly Gly Ser  
 930 935 940  
 Trp Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg  
 945 950 955 960  
 Lys Tyr Gly Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr  
 965 970 975  
 Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly  
 980 985 990  
 Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met  
 995 1000 1005  
 Val Leu Pro Gly Val Ala Asn Ala Asp Lys Met Thr Met Tyr Thr Ala  
 1010 1015 1020  
 Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Ala Val  
 1025 1030 1035 1040  
 Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala  
 1045 1050 1055  
 Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala  
 1060 1065 1070  
 Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn  
 1075 1080 1085  
 Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala Thr Val Ala Lys Ala  
 1090 1095 1100  
 Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser  
 1105 1110 1115 1120  
 His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser  
 1125 1130 1135  
 Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln  
 1140 1145 1150  
 Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val  
 1155 1160 1165  
 Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu  
 1170 1175 1180

Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe  
 1185 1190 1195 1200  
 Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala  
 1205 1210 1215  
 Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr  
 1220 1225 1230  
 Glu Thr Val Thr Ala Trp Ser Gly Ile Cys Ala Ser Asp Gly Asp Arg  
 1235 1240 1245  
 Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn  
 1250 1255 1260  
 Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg  
 1265 1270 1275 1280  
 Val Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu  
 1285 1290 1295  
 Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr  
 1300 1305 1310  
 Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro  
 1315 1320 1325  
 Asn Trp Thr Val Pro Glu Phe Thr Leu Asp Ile Phe Asn Ala Thr Tyr  
 1330 1335 1340  
 Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys  
 1345 1350 1355 1360  
 Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Thr Ile Asn  
 1365 1370 1375  
 Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val  
 1380 1385 1390  
 Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Val Phe  
 1395 1400 1405  
 Cys Ile Pro Leu Leu Leu Phe Cys Cys Phe Ser Thr Gly Cys Cys Gly  
 1410 1415 1420  
 Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg  
 1425 1430 1435 1440  
 Gln Phe Glu Tyr Tyr Glu Pro Ile Glu Lys Val His Val His  
 1445 1450

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2246 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..2244

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

ATG ATT GTG CTC GTA ACT TGC CTC TTG TTA TGT TCA TAC CAC ACA Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr 1 5 10 15	48
GTT TTG AGT ACA ACA AAT AAT GAA TGC ATA CAA GTT AAC GTA ACA CAA Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln 20 25 30	96
TTG GCT GGC AAT GAA AAC CTT ATC AGA GAT TTT CTG TTT AGT AAC TTT Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe 35 40 45	144
AAA GAA GAA GGA AGT GTA GTT GGT GGT TAT TAC CCT ACA GAG GTG Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val 50 55 60	192
TGG TAC AAC TGC TCT AGA ACA GCT CGA ACT ACT GCC TTT CAG TAT TTT Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe 65 70 75 80	240
AAT AAT ATA CAT GCC TTT TAT TTT GTT ATG GAA GCC ATG GAA AAT AGC Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser 85 90 95	288
ACT GGT AAT GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu 100 105 110	336
CCT GTT AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln 115 120 125	384
CAA AGG CCC CTT TTA GAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC Gln Arg Pro Leu Leu Glu His Gly Leu Val Cys Ile Thr Lys Asn Arg 130 135 140	432
CAT ATT AAC TAT GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys 145 150 155 160	480
ACG GGT GCT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn 165 170 175	528
GGA ACA AAA ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala 180 185 190	576
TAT ATT AGT GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe 195 200 205	624
AAC AAT GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GAA Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu 210 215 220	672
TAC AGT GCT GCA TAT GCT TAC CAA GGT GTT TCT AAC TTC ACT TAT TAC Tyr Ser Ala Ala Tyr Ala Tyr Gin Gly Val Ser Asn Phe Thr Tyr Tyr 225 230 235 240	720
AAG TTA AAT AAC ACC AAT GGT CTA AAA ACC TAT GAA TTA TGT GAA GAT Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp 245 250 255	768

TAT GAA CAT TGC ACT GGC TAT GCT ACC AAT GTA TTT GCT CCG ACA TCA Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser 260 265 270	816
GGT GGT TAC ATA CCT GAT GGA TTT AGT TTT AAT AAT TGG TTC TTG CTT Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu 275 280 285	864
ACA AAT AGT TCC ACT TTT GTT AGT GGC AGG TTT GTA ACA AAT CAA CCA Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro 290 295 300	912
TTA TTG ATT AAT TGC TTG TGG CCA GTG CCC AGT TTT GGT GTA GCA GCA Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala 305 310 315 320	960
CAA GAA TTT TGT TTT GAA GGT GCA CAG TTT AGC CAA TGT AAT GGT GTG Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val 325 330 335	1008
TCT TTA AAT AAC ACA GTG GAT GTT ATT AGA TTC AAC CTT AAT TTC ACT Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr 340 345 350	1056
GCA GAT GTA CAA TCT GGT ATG GGT GCC ACA GTA TTT TCA CTG AAT ACA Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr 355 360 365	1104
ACA GGT GGT GTC ATT CTT GAA ATT TCA TGT TAT AGT GAC ACA GTG AGT Thr Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser 370 375 380	1152
GAG TCT AGT TCT TAC AGT TAT GGT GAA ATC CCG TTC GGC ATA ACT GAC Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp 385 390 395 400	1200
GGA CCA CGA TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAA TAT Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr 405 410 415	1248
TTA GGA ACA TTA CCA CCC AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp 420 425 430	1296
GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445	1344
GGT TGT ATA TCT TTT AAT TTA ACC ACT GGT GTT AGT GGA GCT TTT TGG Gly Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp 450 455 460	1392
ACA ATT GCT TAC ACA TCG TAT ACT GAA GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480	1440
ACA GCT ATT AAA AAT GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495	1488
AAA TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510	1536
GCT TCA AGT GAA GTA GGT TTC GTT AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525	1584

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AGC TTT TTC ACA TAC ACC GCT GTC AAT ATA ACC ATT GAT CTT GGT ATG Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met 530 535 540	1632
AAG CTT ACT GGT TAT GGT CAA CCC ATA GCC TCG ACA CTA AGT AAC ATC Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560	1680
ACA CTA CCA ATG CAG GAT AAC AAT ACT GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575	1728
AAC CAA TTC TCA GTT TAT GTT CAT TCC ACT TGC AAA AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp 580 585 590	1776
GAC AAT ATC TTT AAT CAA GAC TGC ACG GAT GTT TTA GAG GCT ACA GCT Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala 595 600 605	1824
GTT ATA AAA ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn 610 615 620	1872
TAC TTG ACT TTT AAC AAG TTC TGT TTG TCG TTG AGT CCT GTT GGT GCT Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640	1920
AAT TGC AAG TTT GAT GTT GCT GCA CGT ACA AGA ACC AAT GAG CAG GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655	1968
GTT AGA AGT CTA TAT GTA ATA TAT GAA GAA GGA GAC AAC ATA GTG GGT Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670	2016
GTA CCG TCT GAT GAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685	2064
GAC TCC TGT ACA GAT TAC AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700	2112
ATT AGA CGA ACT AAC AGT ACG CTA CTT AGT GGC TTA TAT TAC ACA TCA Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser 705 710 715 720	2160
CTA TCA GGT GAT TTG TTA GGC TTT AAA AAT GTT AGT GAT GGT GTC ATT Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile 725 730 735	2208
TAT TCT GTG ACG CCA TGT GAT GTA AGC GCA CAA GCG GC Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala 740 745	2246

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 748 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

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## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr  
1 5 10 15

Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln  
20 25 30

Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe  
35 40 45

Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val  
50 55 60

Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe  
65 70 75 80

Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser  
85 90 95

Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu  
100 105 110

Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln  
115 120 125

Gln Arg Pro Leu Leu Glu His Gly Leu Val Cys Ile Thr Lys Asn Arg  
130 135 140

His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys  
145 150 155 160

Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn  
165 170 175

Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala  
180 185 190

Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe  
195 200 205

Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu  
210 215 220

Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr  
225 230 235 240

Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp  
245 250 255

Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser  
260 265 270

Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu  
275 280 285

Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro  
290 295 300

Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala  
305 310 315 320

Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val  
325 330 335

Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr  
340 345 350

Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr  
355 360 365

Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser  
370 375 380

Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp  
385 390 395 400

Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr  
405 410 415

Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp  
420 425 430

Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile  
435 440 445

Gly Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp  
450 455 460

Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn  
465 470 475 480

Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile  
485 490 495

Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val  
500 505 510

Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro  
515 520 525

Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met  
530 535 540

Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile  
545 550 555 560

Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser  
565 570 575

Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp  
580 585 590

Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala  
595 600 605

Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn  
610 615 620

Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala  
625 630 635 640

Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val  
645 650 655

Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly  
660 665 670

Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu  
675 680 685

Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile  
690 695 700

Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser  
 705 710 715 720  
 Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile  
 725 730 735  
 Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala  
 740 745

## (2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4365 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..4362

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ATG ATT GTG CTC GTA ACT TGC CTC TTG TTG TTA TGT TCA TAC CAC ACA Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr 1 5 10 15	48
GTT TTG AGT ACA ACA AAT AAT GAA TGC ATA CAA GTT AAC GTT ACA CAA Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln 20 25 30	96
TTG GCT GGC AAT GAA AAC CTT ATC AGA GAT TTT CTG TTT AGT AAC TTT Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe 35 40 45	144
AAA GAA GAA GGA AGT GTA GTT GTT GGT TAT TAC CCT ACA GAG GTG Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val 50 55 60	192
TGG TAC AAC TGC TCT AGA ACA GCT CGA ACT ACT GCC TTT CAG TAT TTT Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe 65 70 75 80	240.
AAT AAT ATA CAT GCC TTT TAT TTT GTT ATG GAA GCC ATG GAA AAT AGC Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser 85 90 95	288
ACT GGT AAT GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu 100 105 110	336
CCT GTT AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln 115 120 125	384
CAA AGG CCC CTT TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg 130 135 140	432
CAT ATT AAC TAT GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys 145 150 155 160	480

ACG GGT GCT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn 165 170 175	528
GGA ACA AAA ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala 180 185 190	576
TAT ATT AGT GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe 195 200 205	624
AAC AAT GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GAA Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu 210 215 220	672
TAC AGT GCT GCA TAT GCT TAC CAA GGT GTT TCT AAC TTC ACT TAT TAC Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr 225 230 235 240	720
AAG TTA AAT AAC ACC AAT GGT CTA AAA ACC TAT GAA TTA TGT GAA GAT Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp 245 250 255	768
TAT GAA CAT TGC ACT GGC TAT GCT ACC AAT GTA TTT GCT CCG ACA TCA Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser 260 265 270	816
GGT GGT TAC ATA CCT GAT GGA TTT AGT TTT AAT AAT TGG TTC TTG CTT Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu 275 280 285	864
ACA AAT AGT TCC ACT TTT GTT AGT GGC AGG TTT GTA ACA AAT CAA CCA Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro 290 295 300	912
TTA TTG ATT AAT TGC TTG TGG CCA GTG CCC AGT TTT GGT GTA GTA GCA Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Val Ala 305 310 315 320	960
CAA GAA TTT TGT TTT GAA GGT GCA CAG TTT AGC CAA TGT AAT GGT GTG Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val 325 330 335	1008
TCT TTA AAT AAC ACA GTG GAT GTT ATT AGA TTC AAC CTT AAT TTC ACT Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr 340 345 350	1056
GCA GAT GTA CAA TCT GGT ATG GGT GCT ACA GTA TTT TCA CTG AAT ACA Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr 355 360 365	1104
ACA GGT GGT GTC ATT CTT GAA ATT TCA TGT TAT AGT GAC ACA GTG AGT Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser 370 375 380	1152
GAG TCT AGT TCT TAC AGT TAT GGT GAA ATC CCG TTC GGC ATA ACT GAC Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp 385 390 395 400	1200
GGA CCA CGA TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAA TAT Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr 405 410 415	1248
TTA GGA ACA TTA CCA CCC AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp 420 425 430	1296

GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445	1344
GAT TGT ATA TCT TTT AAT TTA ACC ACT GGT GTT AGT GGA GCT TTT TGG Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp 450 455 460	1392
ACA ATT GCT TAC ACA TCG TAT ACT GAA GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480	1440
ACA GCT ATT AAA AAT GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495	1488
AAA TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510	1536
GCT TCA AGT GAA GTA GGT TTC GTT AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525	1584
AGC TTT TTC ACA TAC ACC GCT GTC AAT ATA ACC ATT GAT CTT GGT ATG Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met 530 535 540	1632
AAG CTT AGT GGT TAT GGT CAA CCC ATA GCC TCG ACA CTA AGT AAC ATC Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560	1680
ACA CTA CCA ATG CAG GAT AAC AAT ACT GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575	1728
AAC CAA TTC TCA GTT TAT GTT CAT TCC ACT TGC AAA AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp 580 585 590	1776
GAC AAT ATT TTT AAT CAA GAC TGC ACG GAT GTT TTA GAG GCT ACA GCT Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala 595 600 605	1824
GTT ATA AAA ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn 610 615 620	1872
TAC TTG ACT TTT AAC ACG TTC TGT TTG TCG TTG AGT CCT GTT GGT GCT Tyr Leu Thr Phe Asn Thr Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640	1920
AAT TGC AAG TTT GAT GTT GCT GCA CGT ACA AGA ACC AAT GAG CAG GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655	1968
GTT AGA AGT CTA TAT ATA ATA TAT GAA GAA GGA GAC AAC ATA GTG GGT Val Arg Ser Leu Tyr Ile Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670	2016
GTA CCG TCT GAT GAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685	2064
GAC TCC TGT ACA GAT TAC AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700	2112

106

ATT AGA CGA ACT AAC AGT ACG CTA CTT AGT GGC TTA TAT TAC ACA TCA Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser 705 710 715 720	2160
CTA TCA GGT GAT TTG TTA GGC TTT AAA AAT GTT AGT GAT GGT GTC ATT Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile 725 730 735	2208
TAT TCT GTG ACG CCA TGT GAT GTA AGC GCA CAA GCG GCT GTT ATT GAT Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp 740 745 750	2256
GGT GCC ATA GTT GGA GCT ATG ACT TCC ATT AAC AGT GAA CTG TTA GGT Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly 755 760 765	2304
CTA ATA CAT TGG ACA ACG ACA CCT AAT TTT TAT TAC TAC TCT ATA TAT Leu Ile His Trp Thr Thr Pro Asn Phe Tyr Tyr Ser Ile Tyr 770 775 780	2352
AAT TAC ACA AGT GAG AGG ACT CGT GGC ACT GCA ATT GAC AGT AAC GAT Asn Tyr Thr Ser Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp 785 790 795 800	2400
GTT GAT TGT GAA CCT GTC ATA ACC TAT TCT AAT ATA GGT GTT TGT AAA Val Asp Cys Glu Pro Val Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys 805 810 815	2448
AAT GGT GCT TTG GTT TTT ATT AAC GTC ACA CAT TCT GAC GGA GAC GTG Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val 820 825 830	2496
CAA CCA ATT AGC ACT GGT AAT GTC ACG ATA CCT ACA AAT TTT ACC ATA Gln Pro Ile Ser Thr Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile 835 840 845	2544
TCT GTG CAA GTT GAA TAC ATG CAG GTT TAC ACT ACA CCA GTA TCA ATA Ser Val Gln Val Glu Tyr Met Gln Val Tyr Thr Thr Pro Val Ser Ile 850 855 860	2592
GAT TGT GCA AGA TAC GTT TGT AAT GGT AAC CCT AGA TGT AAC AAA TTG Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu 865 870 875 880	2640
TTA ACA CAA TAT GTG TCT GCA TGT CAA ACT ATT GAA CAA GCA CTT GCA Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala 885 890 895	2688
ATG GGT GCC AGA CTT GAA AAC ATG GAG GTT GAT TCC ATG TTG TTT GTC Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val 900 905 910	2736
TCG GAA AAT GCC CTT AAA TTG GCA TCT GTT GAG GCG TTC AAT AGT ACA Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr 915 920 925	2784
GAA AAT TTA GAT CCT ATT TAC AAA GAA TGG CCT AGC ATA GGT GGT TCT Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Ser Ile Gly Gly Ser 930 935 940	2832
TGG CTA GGA GGT CTA AAA GAT ATA CTA CCG TCC CAT AAT AGC AAA CGT Trp Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg 945 950 955 960	2880
AAG TAT GGT TCT GCT ATA GAA GAT TTG CTT TTT GAT AAA GTT GTA ACA Lys Tyr Gly Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr 965 970 975	2928

TCT GGT TTA GGT ACA GTT GAT GAA GAT TAT AAA CGT TGT ACT GGT GGT Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly 980 985 990	2976
TAC GAC ATA GCA GAC TTG GTG TGT GCT CAA TAT TAC AAT GGC ATC ATG Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met 995 1000 1005	3024
GTT CTA CCA GGT GTA GCT AAT GCT GAC AAG ATG ACT ATG TAC ACA GCA Val Leu Pro Gly Val Ala Asn Ala Asp Lys Met Thr Met Tyr Thr Ala 1010 1015 1020	3072
TCA CTT GCA GGT GGT ATA ACA TTA GGT GCA CTT GGT GGT GGC GCC GTG Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Ala Val 1025 1030 1035 1040	3120
GCT ATA CCT TTT GCA GTA GCA GTC CAG GCT AGA CTT AAT TAT GTT GCT Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala 1045 1050 1055	3168
CTA CAA ACT GAT GTA TTG AAT AAA AAC CAA CAG ATC CTG GCT AAT GCT Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala 1060 1065 1070	3216
TTC AAT CAA GCT ATT GGT AAC ATT ACA CAG GCT TTT GGT AAG GTT AAT Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn 1075 1080 1085	3264
GAT GCT ATA CAT CAA ACA TCA CAA GGT CTT GCC ACT GTT GCT AAA GCG Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala Thr Val Ala Lys Ala 1090 1095 1100	3312
TTG GCA AAA GTG CAA GAT GTT GTC AAC ACA CAA GGG CAA GCT TTA AGT Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser 1105 1110 1115 1120	3360
CAC CTT ACA GTA CAA TTG CAA AAT AAT TTT CAA GCC ATT AGT AGT TCT His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser 1125 1130 1135	3408
ATT AGT GAT ATT TAT AAC AGG CTT GAC GAA CTG AGT GCT GAT GCA CAA Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln 1140 1145 1150	3456
GTT GAT AGG CTG ATT ACA GGT AGA CTT ACA GCA CTT AAT GCA TTT GTG Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val 1155 1160 1165	3504
TCT CAG ACT CTA ACC AGA CAA GCA GAG GTT AGG GCT AGT AGA CAA CTT Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu 1170 1175 1180	3552
GCC AAA GAC AAG GTT AAT GAA TGT GTT AGG TCT CAG TCT CAG AGA TTC Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe 1185 1190 1195 1200	3600
GGA TTC TGT GGT AAT GGT ACA CAT TTG TTT TCA CTA GCA AAT GCA GCA Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala 1205 1210 1215	3648
CCA AAT GGC ATG ATT TTC TTT CAT ACA GTA CTA TTA CCA ACA GCT TAT Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr 1220 1225 1230	3696
GAA ACT GTA ACA GCT TGG TCA GGT ATT TGT GCT TCA GAT GGC GAT CGC Glu Thr Val Thr Ala Trp Ser Gly Ile Cys Ala Ser Asp Gly Asp Arg 1235 1240 1245	3744

ACT TTC GGA CTT GTC GTT AAA GAT GTG CAG TTG ACG TTG TTT CGT AAT Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn 1250 1255 1260	3792
CTA GAT GAC AAG TTC TAT TTG ACC CCC AGA ACT ATG TAT CAG CCT AGA Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg 1265 1270 1275 1280	3840
GTT GCA ACT AGT TCT GAT TTT GTT CAA ATT GAA GGG TGT GAT GTG TTG Val Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu 1285 1290 1295	3888
TTT GTC AAC GCG ACT GTA ATT GAT TTG CCT AGT ATT ATA CCT GAC TAT Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr 1300 1305 1310	3936
ATT GAC ATT AAT CAA ACT GTT CAA GAC ATA TTA GAA AAT TAC AGA CCA Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro 1315 1320 1325	3984
AAC TGG ACT GTA CCT GAA TTT ACA CTT GAT ATT TTC AAC ACA ACC TAT Asn Trp Thr Val Pro Glu Phe Thr Leu Asp Ile Phe Asn Thr Thr Tyr 1330 1335 1340	4032
TTA AAT CTG ACT GGT GAA ATT GAT GAC TTA GAG TTT AGG TCG GAA AAG Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys 1345 1350 1355 1360	4080
CTA CAT AAC ACT ACA GTA GAA CTT GCC ATT CTC ATT GAT AAC ATT AAT Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Asn Ile Asn 1365 1370 1375	4128
AAT ACA TTA GTC AAT CTT GAA TGG CTC AAT AGA ATT GAA ACT TAT GTA Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val 1380 1385 1390	4176
AAA TGG CCT TGG TAT GTG TGG CTA CTG ATA GGT TTA GTA GTA GTA TTT Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Phe 1395 1400 1405	4224
TGC ATA CCA TTA CTG CTA TTT TGC TGT TTT AGC ACA GGT TGT TGT GGA Cys Ile Pro Leu Leu Phe Cys Cys Phe Ser Thr Gly Cys Cys Gly 1410 1415 1420	4272
TGC ATA GGT TGT TTA GGA AGT TGT TGT CAC TCT ATA TGT AGT AGA AGA Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg 1425 1430 1435 1440	4320
CAA TTT GAA AAT TAT GAA CCA ATT GAA AAA GTG CAT GTC CAC Gln Phe Glu Asn Tyr Glu Pro Ile Glu Lys Val His Val His 1445 1450	4362
TAA	4365

## (2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1454 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr  
 1 5 10 15

Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln  
 20 25 30

Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe  
 35 40 45

Lys Glu Glu Gly Ser Val Val Gly Tyr Tyr Pro Thr Glu Val  
 50 55 60

Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe  
 65 70 75 80

Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser  
 85 90 95

Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu  
 100 105 110

Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln  
 115 120 125

Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg  
 130 135 140

His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys  
 145 150 155 160

Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn  
 165 170 175

Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala  
 180 185 190

Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe  
 195 200 205

Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu  
 210 215 220

Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr  
 225 230 235 240

Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp  
 245 250 255

Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser  
 260 265 270

Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu  
 275 280 285

Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro  
 290 295 300

Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Val Ala  
 305 310 315 320

Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val  
 325 330 335

Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr  
 340 345 350

110

Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr  
 355 360 365  
 Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser  
 370 375 380  
 Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp  
 385 390 395 400  
 Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr  
 405 410 415  
 Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp  
 420 425 430  
 Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile  
 435 440 445  
 Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp  
 450 455 460  
 Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn  
 465 470 475 480  
 Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile  
 485 490 495  
 Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val  
 500 505 510  
 Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro  
 515 520 525  
 Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met  
 530 535 540  
 Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile  
 545 550 555 560  
 Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser  
 565 570 575  
 Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp  
 580 585 590  
 Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala  
 595 600 605  
 Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn  
 610 615 620  
 Tyr Leu Thr Phe Asn Thr Phe Cys Leu Ser Leu Ser Pro Val Gly Ala  
 625 630 635 640  
 Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val  
 645 650 655  
 Val Arg Ser Leu Tyr Ile Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly  
 660 665 670  
 Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu  
 675 680 685  
 Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile  
 690 695 700

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Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser  
 705 710 715 720

Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile  
 725 730 735

Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp  
 740 745 750

Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly  
 755 760 765

Leu Ile His Trp Thr Thr Pro Asn Phe Tyr Tyr Tyr Ser Ile Tyr  
 770 775 780

Asn Tyr Thr Ser Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp  
 785 790 795 800

Val Asp Cys Glu Pro Val Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys  
 805 810 815

Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val  
 820 825 830

Gln Pro Ile Ser Thr Gly Asn Val Thr Ile Pro Thr Asn Phe Thr Ile  
 835 840 845

Ser Val Gln Val Glu Tyr Met Gln Val Tyr Thr Pro Val Ser Ile  
 850 855 860

Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu  
 865 870 875 880

Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala  
 885 890 895

Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val  
 900 905 910

Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr  
 915 920 925

Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Ser Ile Gly Gly Ser  
 930 935 940

Trp Leu Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg  
 945 950 955 960

Lys Tyr Gly Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr  
 965 970 975

Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly  
 980 985 990

Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met  
 995 1000 1005

Val Leu Pro Gly Val Ala Asn Ala Asp Lys Met Thr Met Tyr Thr Ala  
 1010 1015 1020

Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Gly Ala Val  
 1025 1030 1035 1040

Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala  
 1045 1050 1055

112

Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala  
 1060 1065 1070

Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn  
 1075 1080 1085

Asp Ala Ile His Gln Thr Ser Gln Gly Leu Ala Thr Val Ala Lys Ala  
 1090 1095 1100

Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser  
 1105 1110 1115 1120

His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser  
 1125 1130 1135

Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln  
 1140 1145 1150

Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val  
 1155 1160 1165

Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu  
 1170 1175 1180

Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe  
 1185 1190 1195 1200

Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala  
 1205 1210 1215

Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr  
 1220 1225 1230

Glu Thr Val Thr Ala Trp Ser Gly Ile Cys Ala Ser Asp Gly Asp Arg  
 1235 1240 1245

Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn  
 1250 1255 1260

Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg  
 1265 1270 1275 1280

Val Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu  
 1285 1290 1295

Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr  
 1300 1305 1310

Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro  
 1315 1320 1325

Asn Trp Thr Val Pro Glu Phe Thr Leu Asp Ile Phe Asn Thr Thr Tyr  
 1330 1335 1340

Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys  
 1345 1350 1355 1360

Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Asn Ile Asn  
 1365 1370 1375

Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val  
 1380 1385 1390

Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Val Phe  
 1395 1400 1405

Cys Ile Pro Leu Leu Leu Phe Cys Cys Phe Ser Thr Gly Cys Cys Gly  
 1410 1415 1420

Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Ile Cys Ser Arg Arg  
 1425 1430 1435 1440

Gln Phe Glu Asn Tyr Glu Pro Ile Glu Lys Val His Val His  
 1445 1450

## (2) INFORMATION FOR SEQ ID NO:27:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2246 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..2244

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

ATG ATT GTG CTC GTA ACT TGC CTC TTG TTA TGT TCA TAC CAC ACA	48
Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr	
1 5 10 15	
GTT TTG AGT ACA ACA AAT AAT GAA TGC ATA CAA GTT AAC GTA ACA CAA	96
Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln	
20 25 30	
TTG GCT GGC AAT GAA AAC CTT ATC AGA GAT TTT CTG TTT AGT AAC TTT	144
Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe	
35 40 45	
AAA GAA GAA GGA AGT GTA GTT GGT GGT TAT TAC CCT ACA GAG GTG	192
Lys Glu Gly Ser Val Val Gly Gly Tyr Tyr Pro Thr Glu Val	
50 55 60	
TGG TAC AAC TGC TCT AGA ACA GCT CGA ACT ACT GCC TTT CAG TAT TTT	240
Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Ala Phe Gln Tyr Phe	
65 70 75 80	
AAT AAT ATA CAT GCC TTT TAT TTT GTT ATG GAA GCC ATG GAA AAT AGC	288
Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser	
85 90 95	
ACT GGT AAT GCA CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG	336
Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu	
100 105 110	
CCT GTT AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA	384
Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln	
115 120 125	
CAA AGG CCC CTT TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC	432
Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg	
130 135 140	
CAT ATT AAC TAT GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT	480
His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys	
145 150 155 160	

ACG GGT GCT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn 165	170	175	528	
GGA ACA AAA ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala 180	185	190	576	
TAT ATT AGT GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe 195	200	205	624	
AAC AAT GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GAA Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu 210	215	220	672	
TAC AGT GCT GCA TAT GCT TAC CAA GGT GTT TCT AAC TTC ACT TAT TAC Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr 225	230	235	240	720
AAG TTA AAT AAC ACC AAT GGT CTA AAA ACC TAT GAA TTA TGT GAA GAT Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp 245	250	255	768	
TAT GAA CAT TGC ACT GGC TAT GCT ACC AAT GTA TTT GCT CCG ACA TCA Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser 260	265	270	816	
GGT GGT TAC ATA CCT GAT GGA TTT AGT TTT AAT AAT TGG TTC TTG CTT Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu 275	280	285	864	
ACA AAT AGT TCC ACT TTT GTT AGT GGC AGG TTT GTA ACA AAT CAA CCA Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro 290	295	300	912	
TTA TTG ATT AAT TGC TTG TGG CCA GTG CCC AGT TTT GGT GTA GCA GCA Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala 305	310	315	320	960
CAA GAA TTT TGT TTT GAA GGT GCA CAG TTT AGC CAA TGT AAT GGT GTG Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val 325	330	335	1008	
TCT TTA AAT AAC ACA GTG GAT GTT ATT AGA TTC AAC CTT AAT TTC ACT Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr 340	345	350	1056	
GCA GAT GTA CAA TCT GGT ATG GGT GCT ACA GTA TTT TCA CTG AAT ACA Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr 355	360	365	1104	
ACA GGT GGT GTC ATT CTT GAA ATT TCA TGT TAT AGT GAC ACA GTG AGT Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser 370	375	380	1152	
GAG TCT AGT TCT TAC AGT TAT GGT GAA ATC CCG TTC GGC ATA ACT GAC Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp 385	390	395	400	1200
GGA CCA CGA TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAA TAT Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr 405	410	415	1248	
TTA GGA ACA TTA CCA CCC AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp 420	425	430	1296	

GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445	1344
GAT TGT ATA TCT TTT AAT TTA ACC ACT GGT GTT AGT GGA GCT TTT TGG Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp 450 455 460	1392
ACA ATT GCT TAC ACA TCG TAT ACT GAA GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480	1440
ACA GCT ATT AAA AAT GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495	1488
AAA TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510	1536
GCT TCA AGT GAA GTA GGT TTC GTT AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525	1584
AGC TTT TTC ACA TAC ACC GCT GTC AAT ATA ACC ATT GAT CTT GGT ATG Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met 530 535 540	1632
AAG CTT AGT GGT TAT GGT CAA CCC ATA GCC TCG ACA CTA AGT AAC ATC Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560	1680
ACA CTA CCA ATG CAG GAT AAC AAT ACT GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575	1728
AAC CAA TTC TCA GTT TAT GTT CAT TCC ACT TGC AAA AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp 580 585 590	1776
GAC AAT ATT TTT AAT CAA GAC TGC ACG GAT GTT TTA GAG GCT ACA GCT Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala 595 600 605	1824
GTT ATA AAA ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn 610 615 620	1872
TAC TTG ACT TTT AAC AAG TTC TGT TTG TCG TTG AGT CCT GTT GGT GCT Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640	1920
AAT TGC AAG TTT GAT GTT GCT GCA CGT ACA AGA ACC AAT GAG CAG GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655	1968
GTT AGA AGT CTA TAT GTA ATA TAT GAA GAA GGA GAC AAC ATA GTG GGT Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670	2016
GTA CCG TCT GAT GAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685	2064
GAC TCC TGT ACA GAT TAC AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700	2112

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ATT AGA CGA ACT AAC AGT ACG CTA CTT AGT GGC TTA TAT TAC ACA TCA Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser 705 710 715 720	2160
CTA TCA GGT GAT TTG TTA GGC TTT AAA AAT GTT AGT GAT GGT GTC ATT Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile 725 730 735	2208
TAT TCT GTG ACG CCA TGT GAT GTA AGC GCA CAA GCG GC Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala 740 745	2246

## (2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 748 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr 1 5 10 15
Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln 20 25 30
Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe 35 40 45
Lys Glu Glu Gly Ser Val Val Gly Gly Tyr Tyr Pro Thr Glu Val 50 55 60
Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe 65 70 75 80
Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser 85 90 95
Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu 100 105 110
Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln 115 120 125
Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg 130 135 140
His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys 145 150 155 160
Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn 165 170 175
Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala 180 185 190
Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe 195 200 205
Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu 210 215 220

Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr  
225 230 235 240  
Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp  
245 250 255  
Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser  
260 265 270  
Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu  
275 280 285  
Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro  
290 295 300  
Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala  
305 310 315 320  
Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val  
325 330 335  
Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr  
340 345 350  
Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr  
355 360 365  
Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser  
370 375 380  
Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp  
385 390 395 400  
Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr  
405 410 415  
Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp  
420 425 430  
Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile  
435 440 445  
Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp  
450 455 460  
Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn  
465 470 475 480  
Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile  
485 490 495  
Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val  
500 505 510  
Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro  
515 520 525  
Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met  
530 535 540  
Lys Leu Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile  
545 550 555 560  
Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser  
565 570 575

Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp  
 580 585 590  
 Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala  
 595 600 605  
 Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn  
 610 615 620  
 Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala  
 625 630 635 640  
 Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val  
 645 650 655  
 Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly  
 660 665 670  
 Val Pro Ser Asp Asp Ser Gly Leu His Asp Leu Ser Val Leu His Leu  
 675 680 685  
 Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile  
 690 695 700  
 Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser  
 705 710 715 720  
 Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile  
 725 730 735  
 Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala  
 740 745

## (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 370 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 3..368
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG CCT GTT AGT GTT	47
Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val Ser Val	
1 5 10 15	
ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA CAA AGG CCC CTT	95
Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg Pro Leu	
20 25 30	
TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC CAT ATT AAC TAT	143
Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile Asn Tyr	
35 40 45	
GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT ACG GGT GCT GAC	191
Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly Ala Asp	
50 55 60	

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AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT GGA ACA AAA ATC Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr Lys Ile 65                   70                   75	239
TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT TAT ATT AGT GGT Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile Ser Gly 80                   85                   90                   95	287
CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT AAC AAT GTC ACA Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn Val Thr 100               105               110	335
CTT TTG TAT TCA CGC TCA AGC ATT GCT ACC TGG GA Leu Leu Tyr Ser Arg Ser Ser Ile Ala Thr Trp 115               120	370

## (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 122 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val Ser Val Ile 1                   5                   10                   15
Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg Pro Leu Leu 20               25               30
Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile Asn Tyr Glu 35               40               45
Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly Ala Asp Arg 50               55               60
Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr Lys Ile Tyr 65               70               75               80
Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala Tyr Ile Ser Gly Arg 85               90               95
Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn Val Thr Leu 100              105              110
Leu Tyr Ser Arg Ser Ser Ile Ala Thr Trp 115              120

## (2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 4365 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..4362

120

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

ATG ATT GTG CTC GTA ACT TGC CTC TTG TTG TTA TGC TCA TAC CAC ACT Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr	48
1 5 10 15	
GTT TCG AGT ACG TCA AAC AAT GAT TGT AGA CAA GTT AAC GTA ACA CAA Val Ser Ser Thr Ser Asn Asn Asp Cys Arg Gln Val Asn Val Thr Gln	96
20 25 30	
TTA GCT GGC AAT GAA AAC CTT ATT AGA GAC TTT TTG TTT CAA AGT TTT Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Gln Ser Phe	144
35 40 45	
AAA GAA GAA GGA ATT GTA GTT GGT GGT TAT TAC CCT ACA GAG GTG Lys Glu Glu Gly Ile Val Val Gly Gly Tyr Tyr Pro Thr Glu Val	192
50 55 60	
TGG TAC AAC TGC TCT AGA ACA GCA ACT ACC ACT GCC TAT GAG TAT TTT Trp Tyr Asn Cys Ser Arg Thr Ala Thr Thr Ala Tyr Glu Tyr Phe	240
65 70 75 80	
AAT AAT ATA CAT GCC TTT TAT TTT GAT ATG GAA GCT ATG GAA AAT AGC Asn Asn Ile His Ala Phe Tyr Phe Asp Met Glu Ala Met Glu Asn Ser	288
85 90 95	
ACT GGT AAT GCA CGT GGT AAA CCT CTA TTA TTT CAT GTT CAT GGT GAA Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu	336
100 105 110	
CCT GTT AGT ATC ATC ATA TAT ATA TCA GCT TAT GGG GAT GAT GTG CAA Pro Val Ser Ile Ile Tyr Ile Ser Ala Tyr Gly Asp Asp Val Gln	384
115 120 125	
CAA AGG CCA CTT TTA GAA CAT GGG TTA TTG TGC ATT ACT AAA AAT CGC Gln Arg Pro Leu Leu Glu His Gly Leu Leu Cys Ile Thr Lys Asn Arg	432
130 135 140	
AAT ATT GAC TAT AAC ACC TTC ACC AGC AAC CAG TGG GAT TCC ATA TGT Asn Ile Asp Tyr Asn Thr Phe Thr Ser Asn Gln Trp Asp Ser Ile Cys	480
145 150 155 160	
ACG GGT AAT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC AGG GAT AAT Thr Gly Asn Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Arg Asp Asn	528
165 170 175	
GGA ACA AAA ATC TAT GGG CTT GAG TGG AAT GAT GAA TTT GTT ACA GCG Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Glu Phe Val Thr Ala	576
180 185 190	
TAT ATT AGT GGT CGT TCT TAT AAT TGG AAC ATC AAT AAT AAC TGG TTT Tyr Ile Ser Gly Arg Ser Tyr Asn Trp Asn Ile Asn Asn Asn Trp Phe	624
195 200 205	
AAC AAT GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GAA Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu	672
210 215 220	
TAC AGT GCT GCA TAT GTT TAC CAA GGT GTT TCT AAC TTC ACT TAT TAC Tyr Ser Ala Ala Tyr Val Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr	720
225 230 235 240	
AAG TTA AAT AAC ACC AAT GGT TTA AAA ACC TAT GAA TTT TGT GAG GAT Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Phe Cys Glu Asp	768
245 250 255	

TAT GAA TAT TGC ACT GGC TAC GCC ACT AAT GTC TTT GCT CCA ACT GTG Tyr Glu Tyr Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Val 260 265 270	816
GGA GGT TAC ATA CCT GAT GGA TTT AGT TTT AAC AAT TGG TTT TTG CTT Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu 275 280 285	864
ACA AAT AGC TCC ACT TTT GTT AGT GGC AGA TTT GTA ACA AAC CAA CCA Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro 290 295 300	912
CTA TTA GTT AAC TGC TTA TGG CCA GTG CCC AGT TTT GGT GTA GCA GCA Leu Leu Val Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala 305 310 315 320	960
CAA GAA TTT TGT TTT GAA GGT GCG CAG TTT AGT CAG TGT AGT GGT GTA Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Ser Gly Val 325 330 335	1008
TCT TTA AAT AAC ACA GTA GAT GTT ATT AGA TTC AAT CTT AAT TTC ACC Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr 340 345 350	1056
GCA GAT GTA CAA TCT GGT ATG GGT GCT ACA GTG TTT TCG TTG AAT ACA Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr 355 360 365	1104
ACG GGT GGT GTC ATT CTT GAA GTT TCA TGT TAT AAT GAC ACA GTG AGT Thr Gly Val Ile Leu Glu Val Ser Cys Tyr Asn Asp Thr Val Ser 370 375 380	1152
GAG TCT AGT TTT TAC AGT TAT GGT GAA ATT CCG TTC GGC ATA ACT GAT Glu Ser Ser Phe Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp 385 390 395 400	1200
GGA CCA CGG TAC TGT TAT GTA CTT TAC AAT GGC ACA GCT CTT AAG TAT Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr 405 410 415	1248
TTA GGA ACA TTA CCA CCT AGT GTA AAG GAA ATT GCT ATT AGT AAG TGG Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp 420 425 430	1296
GGC CAT TTT TAT ATT AAT GGT TAC AAT TTC TTT AGC ACA TTT CCT ATT Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile 435 440 445	1344
GAT TGT ATA TCT TTT AAC TTA ACC ACT GGT GAT AGT GGA GCT TTT TGG Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Asp Ser Gly Ala Phe Trp 450 455 460	1392
ACA ATT GCT TAC ACA TCG TAC ACT GAG GCA TTA GTA CAA GTT GAA AAC Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn 465 470 475 480	1440
ACA GCT ATT AAA AAG GTG ACG TAT TGT AAC AGT CAC ATT AAT AAC ATT Thr Ala Ile Lys Lys Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile 485 490 495	1488
AAG TGT TCT CAA CTT ACT GCT AAT TTG AAT AAT GGA TTT TAT CCT GTT Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val 500 505 510	1536
GCT TCA AGT GAG GTG GGT CTT GTG AAT AAG AGT GTT GTG TTA TTA CCT Ala Ser Ser Glu Val Gly Leu Val Asn Lys Ser Val Val Leu Leu Pro 515 520 525	1584

ATC TTT TTC GCA CAT ACC GCT ATC AAT ATA ACC ATT GAT CTT GGT ATG Ile Phe Phe Ala His Thr Ala Ile Asn Ile Thr Ile Asp Leu Gly Met 530 535 540	1632
AAG CGT AGC GGT TAT GGT CAA CCC ATA GCA TCA ACA TTA AGT AAC ATT Lys Arg Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile 545 550 555 560	1680
ACA CTA CCA ATG CAG GAT AAT AAC ACA GAT GTG TAC TGT ATT CGT TCT Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser 565 570 575	1728
AAC CAG TTT TCA GTT TAT GTT CAT TCT ATT TGT AAG AGT TCT TTA TGG Asn Gln Phe Ser Val Tyr Val His Ser Ile Cys Lys Ser Ser Leu Trp 580 585 590	1776
GAC AAT ATT TTT AAT CAA GAA TGC ACG GAT GTT TTA GAT GCC ACA GCT Asp Asn Ile Phe Asn Gln Glu Cys Thr Asp Val Leu Asp Ala Thr Ala 595 600 605	1824
GTT ATA AAG ACT GGT ACT TGT CCT TTC TCA TTT GAT AAA TTG AAC AAT Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Asp Lys Leu Asn Asn 610 615 620	1872
TAC TTA ACT TTT AAC AAG TTC TGT TTG TCG TTG AGT CCT GTT GGC GCT Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala 625 630 635 640	1920
AAC TGC AAG TTT GAT GTT GCC GCA CGT ACA AGA ACC AAT GAG CAA GTT Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val 645 650 655	1968
GTT AGA AGT CTA TAT GTA ATA TAT GAA GAA GGA GAC AAC ATA GTT GGT Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly 660 665 670	2016
GTA CCG TCT GAT AAT AGC GGT CTG CAC GAT TTG TCT GTG CTA CAC CTA Val Pro Ser Asp Asn Ser Gly Leu His Asp Leu Ser Val Leu His Leu 675 680 685	2064
GAC TCC TGT ACA GAG TAT AAT ATA TAT GGT AGA ACT GGT GTT GGT ATT Asp Ser Cys Thr Glu Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile 690 695 700	2112
ATT AGA CAA ACT AAC AGT ACG CTA CTT AGC GGC TTA TAT TAC ACA TCA Ile Arg Gln Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser 705 710 715 720	2160
CTA TCA GGT GAT TTG TTA GGC TTT AAA AAT GTT AGT GAT GGT GTC ATC Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile 725 730 735	2208
TAT TCT GTG ACG CCA TGT GAT GTA AGC GCA CAA GCG GCT GTT ATT GAT Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp 740 745 750	2256
GGT GCC ATA GTT GGA GCT ATG ACT TCC ATT AAC AGT GAA CTG TTA GGT Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly 755 760 765	2304
CTA AAA CAC TGG ACA ACA ACA CCT AAT TTT TAT TAC TAC TCT ATA TAT Leu Lys His Trp Thr Thr Pro Asn Phe Tyr Tyr Ser Ile Tyr 770 775 780	2352
AAT TAT ACA AAT GAG AGG ACT CGT GGC ACT GCA ATT GAC AGT AAC GAT Asn Tyr Thr Asn Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp 785 790 795 800	2400

GTT GAT TGT GAA CCT ATC ATA ACC TAT TCT AAC ATA GGT GTT TGT AAA Val Asp Cys Glu Pro Ile Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys 805 810 815	2448
AAT GGT GCT TTG GTT TTT ATT AAC GTC ACA CAT TCT GAT GGA GAC GTG Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val 820 825 830	2496
CAA CCA ATT AGC ACT GGT ACT GTC ACG ATA CCT ACA AAC TTT ACC ATA Gln Pro Ile Ser Thr Gly Thr Val Thr Ile Pro Thr Asn Phe Thr Ile 835 840 845	2544
TCT GTG CAA GTC GAA TAC ATT CAG GTT TAC ACC ACA CCA GTA TCA ATA Ser Val Gln Val Glu Tyr Ile Gln Val Tyr Thr Thr Pro Val Ser Ile 850 855 860	2592
GAT TGT GCA AGA TAC GTT TGC AAT GGT AAC CCT AGA TGT AAC AAA TTG Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu 865 870 875 880	2640
TTA ACA CAA TAT GTT TCT GCA TGT CAA ACT ATT GAG CAA GCA CTT GCA Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala 885 890 895	2688
ATG GGT GCC AGA CTT GAA AAC ATG GAG GTT GAT TCC ATG TTG TTC GTT Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val 900 905 910	2736
TCT GAA AAT GCC CTT AAA TTG GCA TCT GTT GAG GCG TTC AAT AGT ACA Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr 915 920 925	2784
GAA AAT TTA GAC CCT ATT TAC AAA GAA TGG CCT AAC ATA GGT GGT TCT Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Asn Ile Gly Gly Ser 930 935 940	2832
TGG TTA GGA GGT TTA AAA GAC ATA CTG CCG TCC CAT AAT AGC AAA CGT Trp Leu Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg 945 950 955 960	2880
AAG TAT CGT TCT GCT ATA GAA GAC TTG CTT TTT GAT AAG GTT GTA ACT Lys Tyr Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr 965 970 975	2928
TCT GGT TTA GGT ACA GTT GAT GAA GAT TAT AAA CGT TGT ACA GGT GGT Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly 980 985 990	2976
TAT GAC ATA GCC GAC TTA GTG TGT GCT CAA TAT TAC AAT GGC ATC ATG Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met 995 1000 1005	3024
G TG TTA CCT GGT GTA GCT AAT GAT GAC AAG ATG ACT ATG TAC ACA GCA Val Leu Pro Gly Val Ala Asn Asp Asp Lys Met Thr Met Tyr Thr Ala 1010 1015 1020	3072
TCT CTT GCA GGT GGT ATA ACA CTA GGT GCA CTT GGT GGT GGC GCC GTT Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Ala Val 1025 1030 1035 1040	3120
GCT ATA CCT TTT GCA GTA GCA GTT CAA GCT AGA CTT AAT TAT GTT GCT Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala 1045 1050 1055	3168
CTA CAA ACT GAT GTA TTG AAT AAA AAC CAG CAG ATC CTG GCT AAT GCT Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala 1060 1065 1070	3216

TTC AAT CAA GCT ATT GGT AAC ATT ACA CAG GCA TTT GGC AAG GTT AAT Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn 1075 1080 1085	3264
GAT GCT ATA CAT CAA ACA TCA AAA GGT CTT GCA ACT GTT GCT AAA GCA Asp Ala Ile His Gln Thr Ser Lys Gly Leu Ala Thr Val Ala Lys Ala 1090 1095 1100	3312
TTG GCA AAA GTG CAA GAT GTT GTC AAC ACA CAA GGG CAA GCT TTA AGC Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser 1105 1110 1115 1120	3360
CAC CTA ACA GTA CAA TTG CAA AAT AAT TTT CAA GCC ATT AGT AGC TCT His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser 1125 1130 1135	3408
ATT AGT GAT ATT TAT AAC AGG CTT GAC GAA CTG AGT GCT GAT GCA CAA Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln 1140 1145 1150	3456
GTT GAT AGG CTG ATT ACA GGA AGA CTT ACA GCA CTT AAT GCA TTT GTG Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val 1155 1160 1165	3504
TCT CAG ACT CTA ACC AGA CAA GCG GAG GTT AGG GCT AGT AGA CAA CTT Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu 1170 1175 1180	3552
GCC AAG GAC AAG GTT AAT GAA TGT GTT AGA TCC CAA TCT CAG AGA TTT Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe 1185 1190 1195 1200	3600
GGA TTC TGT GGT AAT GGT ACA CAC TTG TTT TCA CTT GCA AAT GCA GCA Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala 1205 1210 1215	3648
CCA AAT GGC ATG ATT TTC TTT CAT ACA GTG CTA TTA CCA ACG GCT TAT Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr 1220 1225 1230	3696
GAA ACT GTA ACA GCT TGG CCA GGT ATT TGT GCT TCA GAT GGC GAT CGC Glu Thr Val Thr Ala Trp Pro Gly Ile Cys Ala Ser Asp Gly Asp Arg 1235 1240 1245	3744
ACT TTT GGA CTT GTC GTT AAA GAT GTA CAG TTG ACG TTG TTT CGT AAC Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn 1250 1255 1260	3792
CTA GAT GAC AAG TTC TAT TTG ACT CCC AGA ACT ATG TAT CAG CCT AGA Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg 1265 1270 1275 1280	3840
GCT GCA ACT AGT TCT GAT TTT GTT CAA ATT GAG GGG TGC GAT GTG TTG Ala Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu 1285 1290 1295	3888
TTT GTC AAT GCA ACT GTA ATT GAC TTG CCT AGT ATT ATA CCT GAC TAT Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr 1300 1305 1310	3936
ATT GAC ATC AAT CAG ACT GTT CAA GAT ATA TTA GAA AAT TAC AGA CCA Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro 1315 1320 1325	3984
AAC TGG ACT GTA CCT GAA TTG ACA CTT GAT ATT TTT AAC GCA ACC TAT Asn Trp Thr Val Pro Glu Leu Thr Leu Asp Ile Phe Asn Ala Thr Tyr 1330 1335 1340	4032

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TTA AAT CTG ACT GGT GAA ATT GAT GAC TTA GAA TTT AGG TCA GAA AAG Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys 1345 1350 1355 1360	4080
CTA CAC AAT ACC ACT GTA GAA CTT GCC ATT CTC ATT GAC AAC ATT AAC Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Asn Ile Asn 1365 1370 1375	4128
AAC ACA TTA GTC AAT CTT GAA TGG CTC AAT AGA ATT GAA ACT TAT GTA Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val 1380 1385 1390	4176
AAA TGG CCT TGG TAT GTG TGG CTA CTA ATA GGC TTA GTA GTA ATA TTT Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Ile Phe 1395 1400 1405	4224
TGC ATA CCA TTA TTG CTA TTT TGC TGT TGT AGT ACA GGT TGT TGT GGA Cys Ile Pro Leu Leu Phe Cys Cys Cys Ser Thr Gly Cys Cys Gly 1410 1415 1420	4272
TGC ATA GGT TGC TTA GGA AGT TGT TGT CAC TCT ATG TGT AGT AGA AGA Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Met Cys Ser Arg Arg 1425 1430 1435 1440	4320
CAA TTT GAA AAT TAT GAA CCA ATT GAA AAA GTG CAT GTC CAC Gln Phe Glu Asn Tyr Glu Pro Ile Glu Lys Val His Val His 1445 1450	4362
TAA	4365

## (2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1454 amino acids
- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Met Ile Val Leu Val Thr Cys Leu Leu Leu Cys Ser Tyr His Thr 1 5 10 15
Val Ser Ser Thr Ser Asn Asn Asp Cys Arg Gln Val Asn Val Thr Gln 20 25 30
Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Gln Ser Phe 35 40 45
Lys Glu Glu Gly Ile Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val 50 55 60
Trp Tyr Asn Cys Ser Arg Thr Ala Thr Thr Ala Tyr Glu Tyr Phe 65 70 75 80
Asn Asn Ile His Ala Phe Tyr Phe Asp Met Glu Ala Met Glu Asn Ser 85 90 95
Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu 100 105 110
Pro Val Ser Ile Ile Ile Tyr Ile Ser Ala Tyr Gly Asp Asp Val Gln 115 120 125

Gln Arg Pro Leu Leu Glu His Gly Leu Leu Cys Ile Thr Lys Asn Arg  
130 135 140

Asn Ile Asp Tyr Asn Thr Phe Thr Ser Asn Gln Trp Asp Ser Ile Cys  
145 150 155 160

Thr Gly Asn Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Arg Asp Asn  
165 170 175

Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Glu Phe Val Thr Ala  
180 185 190

Tyr Ile Ser Gly Arg Ser Tyr Asn Trp Asn Ile Asn Asn Asn Trp Phe  
195 200 205

Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu  
210 215 220

Tyr Ser Ala Ala Tyr Val Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr  
225 230 235 240

Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Phe Cys Glu Asp  
245 250 255

Tyr Glu Tyr Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Val  
260 265 270

Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu  
275 280 285

Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro  
290 295 300

Leu Leu Val Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala  
305 310 315 320

Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Ser Gly Val  
325 330 335

Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr  
340 345 350

Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr  
355 360 365

Thr Gly Gly Val Ile Leu Glu Val Ser Cys Tyr Asn Asp Thr Val Ser  
370 375 380

Glu Ser Ser Phe Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp  
385 390 395 400

Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr  
405 410 415

Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp  
420 425 430

Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile  
435 440 445

Asp Cys Ile Ser Phe Asn Leu Thr Thr Gly Asp Ser Gly Ala Phe Trp  
450 455 460

Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn  
465 470 475 480

Thr Ala Ile Lys Lys Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile  
485 490 495

Lys Cys Ser Gln Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val  
500 505 510

Ala Ser Ser Glu Val Gly Leu Val Asn Lys Ser Val Val Leu Leu Pro  
515 520 525

Ile Phe Phe Ala His Thr Ala Ile Asn Ile Thr Ile Asp Leu Gly Met  
530 535 540

Lys Arg Ser Gly Tyr Gly Gln Pro Ile Ala Ser Thr Leu Ser Asn Ile  
545 550 555 560

Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser  
565 570 575

Asn Gln Phe Ser Val Tyr Val His Ser Ile Cys Lys Ser Ser Leu Trp  
580 585 590

Asp Asn Ile Phe Asn Gln Glu Cys Thr Asp Val Leu Asp Ala Thr Ala  
595 600 605

Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn  
610 615 620

Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala  
625 630 635 640

Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val  
645 650 655

Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly  
660 665 670

Val Pro Ser Asp Asn Ser Gly Leu His Asp Leu Ser Val Leu His Leu  
675 680 685

Asp Ser Cys Thr Glu Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile  
690 695 700

Ile Arg Gln Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser  
705 710 715 720

Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile  
725 730 735

Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala Ala Val Ile Asp  
740 745 750

Gly Ala Ile Val Gly Ala Met Thr Ser Ile Asn Ser Glu Leu Leu Gly  
755 760 765

Leu Lys His Trp Thr Thr Pro Asn Phe Tyr Tyr Ser Ile Tyr  
770 775 780

Asn Tyr Thr Asn Glu Arg Thr Arg Gly Thr Ala Ile Asp Ser Asn Asp  
785 790 795 800

Val Asp Cys Glu Pro Ile Ile Thr Tyr Ser Asn Ile Gly Val Cys Lys  
805 810 815

Asn Gly Ala Leu Val Phe Ile Asn Val Thr His Ser Asp Gly Asp Val  
820 825 830

Gln Pro Ile Ser Thr Gly Thr Val Thr Ile Pro Thr Asn Phe Thr Ile  
 835 840 845  
 Ser Val Gln Val Glu Tyr Ile Gln Val Tyr Thr Thr Pro Val Ser Ile  
 850 855 860  
 Asp Cys Ala Arg Tyr Val Cys Asn Gly Asn Pro Arg Cys Asn Lys Leu  
 865 870 875 880  
 Leu Thr Gln Tyr Val Ser Ala Cys Gln Thr Ile Glu Gln Ala Leu Ala  
 885 890 895  
 Met Gly Ala Arg Leu Glu Asn Met Glu Val Asp Ser Met Leu Phe Val  
 900 905 910  
 Ser Glu Asn Ala Leu Lys Leu Ala Ser Val Glu Ala Phe Asn Ser Thr  
 915 920 925  
 Glu Asn Leu Asp Pro Ile Tyr Lys Glu Trp Pro Asn Ile Gly Gly Ser  
 930 935 940  
 Trp Leu Gly Gly Leu Lys Asp Ile Leu Pro Ser His Asn Ser Lys Arg  
 945 950 955 960  
 Lys Tyr Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp Lys Val Val Thr  
 965 970 975  
 Ser Gly Leu Gly Thr Val Asp Glu Asp Tyr Lys Arg Cys Thr Gly Gly  
 980 985 990  
 Tyr Asp Ile Ala Asp Leu Val Cys Ala Gln Tyr Tyr Asn Gly Ile Met  
 995 1000 1005  
 Val Leu Pro Gly Val Ala Asn Asp Asp Lys Met Thr Met Tyr Thr Ala  
 1010 1015 1020  
 Ser Leu Ala Gly Gly Ile Thr Leu Gly Ala Leu Gly Gly Ala Val  
 1025 1030 1035 1040  
 Ala Ile Pro Phe Ala Val Ala Val Gln Ala Arg Leu Asn Tyr Val Ala  
 1045 1050 1055  
 Leu Gln Thr Asp Val Leu Asn Lys Asn Gln Gln Ile Leu Ala Asn Ala  
 1060 1065 1070  
 Phe Asn Gln Ala Ile Gly Asn Ile Thr Gln Ala Phe Gly Lys Val Asn  
 1075 1080 1085  
 Asp Ala Ile His Gln Thr Ser Lys Gly Leu Ala Thr Val Ala Lys Ala  
 1090 1095 1100  
 Leu Ala Lys Val Gln Asp Val Val Asn Thr Gln Gly Gln Ala Leu Ser  
 1105 1110 1115 1120  
 His Leu Thr Val Gln Leu Gln Asn Asn Phe Gln Ala Ile Ser Ser Ser  
 1125 1130 1135  
 Ile Ser Asp Ile Tyr Asn Arg Leu Asp Glu Leu Ser Ala Asp Ala Gln  
 1140 1145 1150  
 Val Asp Arg Leu Ile Thr Gly Arg Leu Thr Ala Leu Asn Ala Phe Val  
 1155 1160 1165  
 Ser Gln Thr Leu Thr Arg Gln Ala Glu Val Arg Ala Ser Arg Gln Leu  
 1170 1175 1180  
 Ala Lys Asp Lys Val Asn Glu Cys Val Arg Ser Gln Ser Gln Arg Phe

129

1185	1190	1195	1200
Gly Phe Cys Gly Asn Gly Thr His Leu Phe Ser Leu Ala Asn Ala Ala			
1205		1210	1215
Pro Asn Gly Met Ile Phe Phe His Thr Val Leu Leu Pro Thr Ala Tyr			
1220	1225	1230	
Glu Thr Val Thr Ala Trp Pro Gly Ile Cys Ala Ser Asp Gly Asp Arg			
1235	1240	1245	
Thr Phe Gly Leu Val Val Lys Asp Val Gln Leu Thr Leu Phe Arg Asn			
1250	1255	1260	
Leu Asp Asp Lys Phe Tyr Leu Thr Pro Arg Thr Met Tyr Gln Pro Arg			
1265	1270	1275	1280
Ala Ala Thr Ser Ser Asp Phe Val Gln Ile Glu Gly Cys Asp Val Leu			
1285	1290	1295	
Phe Val Asn Ala Thr Val Ile Asp Leu Pro Ser Ile Ile Pro Asp Tyr			
1300	1305	1310	
Ile Asp Ile Asn Gln Thr Val Gln Asp Ile Leu Glu Asn Tyr Arg Pro			
1315	1320	1325	
Asn Trp Thr Val Pro Glu Leu Thr Leu Asp Ile Phe Asn Ala Thr Tyr			
1330	1335	1340	
Leu Asn Leu Thr Gly Glu Ile Asp Asp Leu Glu Phe Arg Ser Glu Lys			
1345	1350	1355	1360
Leu His Asn Thr Thr Val Glu Leu Ala Ile Leu Ile Asp Asn Ile Asn			
1365	1370	1375	
Asn Thr Leu Val Asn Leu Glu Trp Leu Asn Arg Ile Glu Thr Tyr Val			
1380	1385	1390	
Lys Trp Pro Trp Tyr Val Trp Leu Leu Ile Gly Leu Val Val Ile Phe			
1395	1400	1405	
Cys Ile Pro Leu Leu Leu Phe Cys Cys Cys Ser Thr Gly Cys Cys Gly			
1410	1415	1420	
Cys Ile Gly Cys Leu Gly Ser Cys Cys His Ser Met Cys Ser Arg Arg			
1425	1430	1435	1440
Gln Phe Glu Asn Tyr Glu Pro Ile Glu Lys Val His Val His			
1445	1450		

## (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 2246 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown
  
- (ii) MOLECULE TYPE: cDNA
  
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..2244

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

ATGATTGTGC TCGTAACTTG CCTCTTGTG TTATGTTCAT ACCACACAGT TTTGAGTACA	60
ACAAATAATG AATGCATACA AGTTAACGTA ACACAAATTGG CTGGCAATGA AAACCTTATC	120
AGAGATTTTC TGTTTAGTAA CTTAAAGAA GAAGGAAGTG TAGTTGTTGG TGGTTATTAC	180
CCTACAGAGG TGTGGTACAA CTGCTCTAGA ACAGCTCGAA CTACTGCCCT TCAGTATTTC	240
AATAATATAC ATGCCTTTA TTTGTTATG GAAGCCATGG AAAATAGCAC TGGTAATGCA	300
CGTGGTAAAC CATTATTATT TCATGTGCAT GGTGAGCCTG TTAGTGTAT TATATATATA	360
TCGGCTTATA GGGATGATGT GCAACAAAGG CCCCTTTAA AACATGGTT AGTGTGCATA	420
ACTAAAAATC GCCATATTAA CTATGAACAA TTCACCTCCA ACCAGTGGAA TTCCACATGT	480
ACGGGTGCTG ACAGAAAAAT TCCTTCTCT GTCAACACCA CGGACAATGG AACAAAAATC	540
TATGGTCTTG AGTGAATGA TGACTTTGTT ACAGCTTATA TTAGTGGTCG TTCTTATCAC	600
TTGAACATCA ATACTAATTG GTTAAACAAT GTCACACTT TGTATTCACTG CTCAAGCACT	660
GCTACCTGGG AATACAGTGC TGCATATGCT TACCAAGGTG TTTCTAACTT CACTTATTAC	720
AAGTTAAATA ACACCAATGG TCTAAAACC TATGAATTAT GTGAAGATTA TGAACATTGC	780
ACTGGCTATG CTACCAATGT ATTTGCTCCG ACATCAGGTG GTTACATACC TGATGGATTT	840
AGTTTAAYA ATTGGTTCTT GCTTACAAAT AGTTCCACTT TTGTTAGTGG CAGGTTTGT	900
ACAAATCAAC CATTATTGAT TAATTGCTTG TGGCCAGTGC CCAGTTTGG TGTAGCAGCA	960
CAAGAATTTC GTTTGAAGG TGCACAGTT AGCCAATGTA ATGGTGTGTC TTTAAATAAC	1020
ACAGTGGATG TTATTAGATT CAACCTTAAT TTCACTGCAG ATGTACAATC TGGTATGGGT	1080
GCTACAGTAT TTCACTGAA TACAACAGGT GGTGTCAATT TTGAAATTTC ATGTTATAGT	1140
GACACAGTGA GTGAGTCTAG TTCTTACAGT TATGGTAAA TCCC GTTCGG CATAACTGAC	1200
GGACCACGAT ACTGTTATGT ACTTTACAAT GGACAGCTC TTAAATATTT AGGAACATTA	1260
CCACCCAGTG TAAAGGAAAT TGCTATTAGT AAGTGGGGCC ATTTTATAT TAATGGTTAC	1320
AATTCTTTA GCACATTCC TATTGRTTGT ATATCTTTA ATTTAACAC TGGTGTAGT	1380
GGAGCTTTT GGACAATTGC TTACACATCG TATACTGAAG CATTAGTACA AGTGAAAC	1440
ACAGCTATTA AAAATGTGAC GTATTGTAAC AGTCACATTA ATAACATTAA ATGTTCTCAA	1500
CTTACTGCTA ATTTGAATAA TGGATTTAT CCTGTTGCTT CAAGTGAAGT AGGTTTCGTT	1560
AATAAGAGTG TTGTGTATT ACCTAGCTT TTCACATACA CCGCTGTCAA TATAACCATT	1620
GATCTGGTA TGAAGCTTAG TGGTTATGGT CAACCCATAG CCTCGACACT AAGTAACATC	1680
ACACTACCAA TGCAGGATAA CAATACTGAT GTGTACTGTA TTCGTTCTAA CCAATTCTCA	1740
GTTCATGTTC ATTCCACTTG CAAAAGTTCT TTATGGGACA ATATTTTAA TCAAGACTGC	1800
ACGGATGTTT TAGAGGCTAC AGCTGTTATA AAAACTGGTA CTTGTCCTT CTCATTGAT	1860
AAATTGAACA ATTACTTGAC TTTAACAAAG TTCTGTTGT CGTGAGTCC TGTGGTGCT	1920
AATTGCAAGT TTGATGTTGC TGCACGTACA AGAACCAATG AGCAGGTTGT TAGAAGTCTA	1980

TATGTAATAT ATGAAGAAGG AGACAAACATA GTGGGTGTAC CGTCTGATRA TAGCGGTCTG	2040
CACGATTTGT CTGTGCTACA CCTAGACTCC TGTACAGATT ACAATATATA TGGTAGAACT	2100
GGTGTTGGTA TTATTAGACG AACTAACAGT ACGCTACTTA GTGGCTTATA TTACACATCA	2160
CTATCAGGTG ATTTGTTAGG CTTTAAAAAT GTTAGTGATG GTGTCATTTA TTCTGTGACG	2220
CCATGTGATG TAAGCGCACA AGCGGC	2246

## (2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 748 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Met Ile Val Leu Val Thr Cys Leu Leu Leu Leu Cys Ser Tyr His Thr	
1 5 10 15	
Val Leu Ser Thr Thr Asn Asn Glu Cys Ile Gln Val Asn Val Thr Gln	
20 25 30	
Leu Ala Gly Asn Glu Asn Leu Ile Arg Asp Phe Leu Phe Ser Asn Phe	
35 40 45	
Lys Glu Glu Gly Ser Val Val Val Gly Gly Tyr Tyr Pro Thr Glu Val	
50 55 60	
Trp Tyr Asn Cys Ser Arg Thr Ala Arg Thr Thr Ala Phe Gln Tyr Phe	
65 70 75 80	
Asn Asn Ile His Ala Phe Tyr Phe Val Met Glu Ala Met Glu Asn Ser	
85 90 95	
Thr Gly Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu	
100 105 110	
Pro Val Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln	
115 120 125	
Gln Arg Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg	
130 135 140	
His Ile Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys	
145 150 155 160	
Thr Gly Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn	
165 170 175	
Gly Thr Lys Ile Tyr Gly Leu Glu Trp Asn Asp Asp Phe Val Thr Ala	
180 185 190	
Tyr Ile Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe	
195 200 205	
Asn Asn Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp Glu	
210 215 220	
Tyr Ser Ala Ala Tyr Ala Tyr Gln Gly Val Ser Asn Phe Thr Tyr Tyr	
225 230 235 240	

Lys Leu Asn Asn Thr Asn Gly Leu Lys Thr Tyr Glu Leu Cys Glu Asp  
 245 250 255  
 Tyr Glu His Cys Thr Gly Tyr Ala Thr Asn Val Phe Ala Pro Thr Ser  
 260 265 270  
 Gly Gly Tyr Ile Pro Asp Gly Phe Ser Phe Asn Asn Trp Phe Leu Leu  
 275 280 285  
 Thr Asn Ser Ser Thr Phe Val Ser Gly Arg Phe Val Thr Asn Gln Pro  
 290 295 300  
 Leu Leu Ile Asn Cys Leu Trp Pro Val Pro Ser Phe Gly Val Ala Ala  
 305 310 315 320  
 Gln Glu Phe Cys Phe Glu Gly Ala Gln Phe Ser Gln Cys Asn Gly Val  
 325 330 335  
 Ser Leu Asn Asn Thr Val Asp Val Ile Arg Phe Asn Leu Asn Phe Thr  
 340 345 350  
 Ala Asp Val Gln Ser Gly Met Gly Ala Thr Val Phe Ser Leu Asn Thr  
 355 360 365  
 Thr Gly Gly Val Ile Leu Glu Ile Ser Cys Tyr Ser Asp Thr Val Ser  
 370 375 380  
 Glu Ser Ser Ser Tyr Ser Tyr Gly Glu Ile Pro Phe Gly Ile Thr Asp  
 385 390 395 400  
 Gly Pro Arg Tyr Cys Tyr Val Leu Tyr Asn Gly Thr Ala Leu Lys Tyr  
 405 410 415  
 Leu Gly Thr Leu Pro Pro Ser Val Lys Glu Ile Ala Ile Ser Lys Trp  
 420 425 430  
 Gly His Phe Tyr Ile Asn Gly Tyr Asn Phe Phe Ser Thr Phe Pro Ile  
 435 440 445  
 Xaa Cys Ile Ser Phe Asn Leu Thr Thr Gly Val Ser Gly Ala Phe Trp  
 450 455 460  
 Thr Ile Ala Tyr Thr Ser Tyr Thr Glu Ala Leu Val Gln Val Glu Asn  
 465 470 475 480  
 Thr Ala Ile Lys Asn Val Thr Tyr Cys Asn Ser His Ile Asn Asn Ile  
 485 490 495  
 Lys Cys Ser Gin Leu Thr Ala Asn Leu Asn Asn Gly Phe Tyr Pro Val  
 500 505 510  
 Ala Ser Ser Glu Val Gly Phe Val Asn Lys Ser Val Val Leu Leu Pro  
 515 520 525  
 Ser Phe Phe Thr Tyr Thr Ala Val Asn Ile Thr Ile Asp Leu Gly Met  
 530 535 540  
 Lys Leu Ser Gly Tyr Gly Gin Pro Ile Ala Ser Thr Leu Ser Asn Ile  
 545 550 555 560  
 Thr Leu Pro Met Gln Asp Asn Asn Thr Asp Val Tyr Cys Ile Arg Ser  
 565 570 575  
 Asn Gln Phe Ser Val Tyr Val His Ser Thr Cys Lys Ser Ser Leu Trp  
 580 585 590

133

Asp Asn Ile Phe Asn Gln Asp Cys Thr Asp Val Leu Glu Ala Thr Ala  
 595 600 605

Val Ile Lys Thr Gly Thr Cys Pro Phe Ser Phe Asp Lys Leu Asn Asn  
 610 615 620

Tyr Leu Thr Phe Asn Lys Phe Cys Leu Ser Leu Ser Pro Val Gly Ala  
 625 630 635 640

Asn Cys Lys Phe Asp Val Ala Ala Arg Thr Arg Thr Asn Glu Gln Val  
 645 650 655

Val Arg Ser Leu Tyr Val Ile Tyr Glu Glu Gly Asp Asn Ile Val Gly  
 660 665 670

Val Pro Ser Asp Xaa Ser Gly Leu His Asp Leu Ser Val Leu His Leu  
 675 680 685

Asp Ser Cys Thr Asp Tyr Asn Ile Tyr Gly Arg Thr Gly Val Gly Ile  
 690 695 700

Ile Arg Arg Thr Asn Ser Thr Leu Leu Ser Gly Leu Tyr Tyr Thr Ser  
 705 710 715 720

Leu Ser Gly Asp Leu Leu Gly Phe Lys Asn Val Ser Asp Gly Val Ile  
 725 730 735

Tyr Ser Val Thr Pro Cys Asp Val Ser Ala Gln Ala  
 740 745

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..27

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TCG AGT ACG TCA AAC AAT GAT TGT AGA  
 Ser Ser Thr Ser Asn Asn Asp Cys Arg  
 1 5

27

## (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Ser Thr Ser Asn Asn Asp Cys Arg  
 1 5

## (2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CAA AGT TTT AAA GAA GGA ATT  
Gln Ser Phe Lys Glu Gly Ile  
1 5

24

## (2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gln Ser Phe Lys Glu Glu Gly Ile  
1 5

## (2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
(B) LOCATION: 1..18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCA ACT ACC ACT GCC TAT  
Ala Thr Thr Thr Ala Tyr  
1 5

18

## (2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Ala Thr Thr Thr Ala Tyr  
 1                   5

## (2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 150 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..150

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GGG GAT GAT GTG CAA CAA AGG CCA CTT TTA GAA CAT GGG TTA TTG TGC	48
Gly Asp Asp Val Gln Gln Arg Pro Leu Leu Glu His Gly Leu Leu Cys	
1                   5                   10                   15	
ATT ACT AAA AAT CGC AAT ATT GAC TAT AAC ACC TTC ACC AGC AAC CAG	96
Ile Thr Lys Asn Arg Asn Ile Asp Tyr Asn Thr Phe Thr Ser Asn Gln	
20                   25                   30	
TGG GAT TCC ATA TGT ACG GGT AAT GAC AGA AAA ATT CCT TTC TCT GTC	144
Trp Asp Ser Ile Cys Thr Gly Asn Asp Arg Lys Ile Pro Phe Ser Val	
35                   40                   45	
ATA CCC	150
Ile Pro	
50	

## (2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 50 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Gly Asp Asp Val Gln Gln Arg Pro Leu Leu Glu His Gly Leu Leu Cys	
1                   5                   10                   15	
Ile Thr Lys Asn Arg Asn Ile Asp Tyr Asn Thr Phe Thr Ser Asn Gln	
20                   25                   30	
Trp Asp Ser Ile Cys Thr Gly Asn Asp Arg Lys Ile Pro Phe Ser Val	
35                   40                   45	
Ile Pro	
50	

## (2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 18 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

AAT ATT GAC TAT AAC ACC  
 Asn Ile Asp Tyr Asn Thr  
 1 5

18

## (2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 6 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Asn Ile Asp Tyr Asn Thr  
 1 5

## (2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 66 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION: 1..66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTG TGC ATT ACT AAA AAT CGC AAT ATT GAC TAT AAC ACC TTC ACC AGC  
 Leu Cys Ile Thr Lys Asn Arg Asn Ile Asp Tyr Asn Thr Phe Thr Ser  
 1 5 10 15

48

AAC CAG TGG GAT TCC ATA  
 Asn Gln Trp Asp Ser Ile  
 20

66

## (2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Leu Cys Ile Thr Lys Asn Arg Asn Ile Asp Tyr Asn Thr Phe Thr Ser  
1 5 10 15

Asn Gln Trp Asp Ser Ile  
20

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..24

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AAT CGC AAT ATT GAC TAT AAC ACC  
Asn Arg Asn Ile Asp Tyr Asn Thr  
1 5

24

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Asn Arg Asn Ile Asp Tyr Asn Thr  
1 5

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..18

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

AAT TGG AAC ATC AAT AAT  
Asn Trp Asn Ile Asn Asn  
1 5

18

## (2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 6 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Asn Trp Asn Ile Asn Asn  
1 5

## (2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 24 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..24
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ATC TTT TTC GCA CAT ACC GCT ATC  
Ile Phe Phe Ala His Thr Ala Ile  
1 5

24

## (2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: unknown
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Ile Phe Phe Ala His Thr Ala Ile  
1 5

## (2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 377 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..375

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

AAT GCT CGT GGT AAA CCA TTA TTA TTT CAT GTG CAT GGT GAG CCT GTT Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val 1 5 10 15	48
AGT GTT ATT ATA TAT ATA TCG GCT TAT AGG GAT GAT GTG CAA CAA AGG Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg 20 25 30	96
CCC CTT TTA AAA CAT GGG TTA GTG TGC ATA ACT AAA AAT CGC CAT ATT Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile 35 40 45	144
AAC TAT GAA CAA TTC ACC TCC AAC CAG TGG AAT TCC ACA TGT ACG GGT Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly 50 55 60	192
GCT GAC AGA AAA ATT CCT TTC TCT GTC ATA CCC ACG GAC AAT GGA ACA Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr 65 70 75 80	240
AAA ATC TAT GGT CTT GAG TGG AAT GAT GAC TTT GTT ACA GCT TAT ATT Lys Ile Tyr Gly Leu Glu Trp Asn Asp Phe Val Thr Ala Tyr Ile 85 90 95	288
AGT GGT CGT TCT TAT CAC TTG AAC ATC AAT ACT AAT TGG TTT AAC AAT Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn 100 105 110	336
GTC ACA CTT TTG TAT TCA CGC TCA AGC ACT GCT ACC TGG GA Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp 115 120 125	377

## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asn Ala Arg Gly Lys Pro Leu Leu Phe His Val His Gly Glu Pro Val 1 5 10 15	
Ser Val Ile Ile Tyr Ile Ser Ala Tyr Arg Asp Asp Val Gln Gln Arg 20 25 30	
Pro Leu Leu Lys His Gly Leu Val Cys Ile Thr Lys Asn Arg His Ile 35 40 45	
Asn Tyr Glu Gln Phe Thr Ser Asn Gln Trp Asn Ser Thr Cys Thr Gly 50 55 60	
Ala Asp Arg Lys Ile Pro Phe Ser Val Ile Pro Thr Asp Asn Gly Thr 65 70 75 80	
Lys Ile Tyr Gly Leu Glu Trp Asn Asp Phe Val Thr Ala Tyr Ile 85 90 95	

140

Ser Gly Arg Ser Tyr His Leu Asn Ile Asn Thr Asn Trp Phe Asn Asn  
100 105 110

Val Thr Leu Leu Tyr Ser Arg Ser Ser Thr Ala Thr Trp  
115 120 125